

## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/234,208D  
Source: IFW/6  
Date Processed by STIC: 12/3/04

***ENTERED***



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/234,208D

DATE: 12/03/2004

TIME: 10:26:03

Input Set : A:\09234208 SEQ LIST.txt  
 Output Set: N:\CRF4\12032004\I234208D.raw

3 <110> APPLICANT: Doherty, Joni Kristin  
 4 Clinton, Gail M.  
 6 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS  
 8 <130> FILE REFERENCE: 49321-1  
 10 <140> CURRENT APPLICATION NUMBER: 09/234,208D  
 11 <141> CURRENT FILING DATE: 1999-01-20  
 13 <160> NUMBER OF SEQ ID NOS: 12  
 15 <170> SOFTWARE: PatentIn version 3.2  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 79  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Homo sapiens  
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 25 1 5 10 15  
 28 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro  
 29 20 25 30  
 32 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu  
 33 35 40 45  
 36 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro  
 37 50 55 60  
 40 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly  
 41 65 70 75  
 44 <210> SEQ ID NO: 2  
 45 <211> LENGTH: 419  
 46 <212> TYPE: PRT  
 47 <213> ORGANISM: Homo sapiens  
 49 <400> SEQUENCE: 2  
 51 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu  
 52 1 5 10 15  
 55 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys  
 56 20 25 30  
 59 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
 60 35 40 45  
 63 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
 64 50 55 60  
 67 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
 68 65 70 75 80  
 71 Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu  
 72 85 90 95  
 75 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr  
 76 100 105 110  
 79 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro

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80	115	120	125
83	Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser		
84	130	135	140
87	Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln		
88	145	150	155
91	Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn		160
92	165	170	175
95	Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys		
96	180	185	190
99	His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser		
100	195	200	205
103	Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys		
104	210	215	220
107	Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys		
108	225	230	235
111	240	245	255
112	Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu		
115	255	260	270
116	His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val		
119	270	275	285
120	Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg		
123	285	290	295
124	Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu		
127	300	305	310
128	Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln		
131	315	320	325
132	Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys		
135	330	335	340
136	Pro Cys Ala Arg Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala Val		
139	345	350	355
140	Pro Val Pro Leu Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser		
143	360	365	370
144	Phe Leu Arg Pro Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro		
147	375	380	385
148	Leu Ala Pro Leu Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val		
151	395	400	405
152	Gly Arg Gly Pro Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg		
155	410	415	415
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160	<211> LENGTH: 19		
161	<212> TYPE: DNA		
162	<213> ORGANISM: artificial sequence		
164	<220> FEATURE:		
165	<223> OTHER INFORMATION: primer		
167	<400> SEQUENCE: 3		19
168	tgagcaccat ggagctggc		
171	<210> SEQ ID NO: 4		
172	<211> LENGTH: 22		
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174 <213> ORGANISM: artificial sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: primer
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184 <211> LENGTH: 22
185 <212> TYPE: DNA
186 <213> ORGANISM: artificial sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: primer
191 <400> SEQUENCE: 5
192 aacacagcgg tgtgagaagt gc 22
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 21
197 <212> TYPE: DNA
198 <213> ORGANISM: artificial sequence
200 <220> FEATURE:
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203 <400> SEQUENCE: 6
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207 <210> SEQ ID NO: 7
208 <211> LENGTH: 20
209 <212> TYPE: DNA
210 <213> ORGANISM: artificial sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: primer
215 <400> SEQUENCE: 7
216 tctgggtacc cactcaactgc 20
219 <210> SEQ ID NO: 8
220 <211> LENGTH: 22
221 <212> TYPE: DNA
222 <213> ORGANISM: artificial sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: primer
227 <400> SEQUENCE: 8
228 ttccacactgg cacgtccaga cc 22
231 <210> SEQ ID NO: 9
232 <211> LENGTH: 27
233 <212> TYPE: DNA
234 <213> ORGANISM: artificial sequence
236 <220> FEATURE:
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243 <210> SEQ ID NO: 10
244 <211> LENGTH: 287
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
  
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Input Set : A:\09234208 SEQ LIST.txt  
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248 <400> SEQUENCE: 10  
249 cccgaggtac ccactcaactg ctcccgaggc cagctgcagt tcctgtccct ctgcgcattgc 60  
251 agcctggccc agccccccct gtcctatctt tcctcagacc ctcttgggac ctatgtctctg 120  
253 ccttctactc tctacccttg gcctttctca gccttccacaag tgccctata tccctgtca 180  
255 gtgtggggag gggccggac cctgatgttc atgtggctgt taacctgtcc cggtatgaag 240  
257 gctgagacgg cccctttttt cacccttccca caccttctca gtgtgt 287  
260 <210> SEQ ID NO: 11  
261 <211> LENGTH: 276  
262 <212> TYPE: DNA  
263 <213> ORGANISM: Homo sapiens  
266 <220> FEATURE:  
267 <221> NAME/KEY: CDS  
268 <222> LOCATION: (1)..(240)  
269 <223> OTHER INFORMATION: ECDIIIa intron-encoded region of herstatin  
271 <400> SEQUENCE: 11  
272 ggt acc cac tca ctg ctc ccg agg cca gct gca gtt cct gtc cct ctg 48  
273 Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala Val Pro Val Pro Leu  
274 1 5 10 15  
276 cgc atg cag cct ggc cca gcc cac cct gtc cta tcc ttc ctc aga ccc 96  
277 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro  
278 20 25 30  
280 tct tgg gac cta gtc tct gcc ttc tac tct cta ccc ctg gcc ccc ctc 144  
281 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu  
282 35 40 45  
284 agc ccc aca agt gtc cct ata tcc cct gtc agt gtg ggg agg ggc ccg 192  
285 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro  
286 50 55 60  
288 gac cct gat gct cat gtg gct gtt aac ctg tcc cgg tat gaa ggc tga 240  
289 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly  
290 65 70 75  
292 gacggccct tccccaccc acccccaccc cctcag 276  
295 <210> SEQ ID NO: 12  
296 <211> LENGTH: 79  
297 <212> TYPE: PRT  
298 <213> ORGANISM: Homo sapiens  
300 <400> SEQUENCE: 12  
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306 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro  
307 20 25 30  
310 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu  
311 35 40 45  
314 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro  
315 50 55 60  
318 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly  
319 65 70 75

**VERIFICATION SUMMARY**

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